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**FIGURE 363**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTC  
CCAGGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGA  
AGAGGGATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTT  
GGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGT  
GCCCTGGTTCTTGCTGTCTTGGCACTGGGCGGAAGCCAGTGGTCCTTTCTCTGGAGAG  
GCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGA  
CAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCC  
TACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTG  
TCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGA  
AAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGC  
CCAAGTCGTGCTCTCCTTCCAGGCCTACCCACTGCCCCGTGCGTCTGCTGGAGGTGCA  
AGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGACTGCTT  
CGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTATACTCAGCCCAGGTACGAGAA  
GGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGG  
TGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTA  
CTGGAATCAGTCCAGGGCCCCCCTAAACCCCGGTGGCACAAAAACCTGACTGGACCGCA  
GATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTGAGGTGTGGCCTCT  
GGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCCCGGCACACCA  
GAACCTCTGGCAAGCCGCCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGACGC  
ACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTG  
CCAGCCACTGGTCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT  
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGGTGAACAGCTCGGAGAAGCTGCA  
GCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTT  
GGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTAC  
TTCCTACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGA  
CCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTT  
TGCCGCTGCGCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAG  
GCTCTTGAAACAGGACGTCCGCTCGGGGGCGGCCGACGGGGCCGCGCGGCTCTGCTCCT  
CTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTGGGCGCCCTGGCGTCCGCCCTGTG  
CCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGG  
GCCCCGTGGCTTGGTTTACGCGCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGGT  
CTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTG  
CGGGCCCCGGGGCGCACGGCCCCGACGACGCTTCCGCGCCTCGCTCAGCTGCGTGCTGCC  
CGACTTCTTGACAGGGCCGGGCGCCCCGGCAGCTACGTGGGGGCCTGCTTCGACAGGCTGCT  
CCACCCGGACGCCGTACCCGCCCTTTTCCGACCCGTGCCCGTCTTCACACTGCCCTCCCA  
ACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCGGGCGGCTCCA  
AGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTCCATCC  
CCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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**FIGURE 364**

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWDS DILCLPGDIVPAPGPV  
LAPTHLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS  
LQAQVVLSTFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR  
YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPVKPRWHKNLT  
GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL  
LDAPCSLPAAEALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE  
KLQEQECLWADSLGPLKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRAARLGEYL  
LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLKKDHAKG  
WLRLKQDVRS GAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS  
AQQPVAVFHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC  
VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQQPRAPRSG  
RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**  
amino acids 1-20

**Transmembrane domain:**  
amino acids 453-475

**N-glycosylation sites:**  
amino acids 118-121, 186-189, 198-201, 211-214, 238-241,  
248-251, 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site:**  
amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**  
amino acids 552-555

**N-myristoylation sites:**  
amino acids 107-112, 152-157, 319-324, 438-443, 516-521,  
612-617, 692-697, 696-701, 700-705

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## FIGURE 365

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCGGCTGACTGCGCCTCTGC  
TTTCTTTCCATAACCTTTTCTTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTC  
CGGACACTAGGGTGCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAAC  
CATGCTGCCGCGCGCGGGCCCGCAGCTGCCTTGCGCTGCCTGTGCTCCTGCTACTGCT  
GGTGGTGCTGACGCCGCCCCGACCGGCGCAAGGCCATCCCCAGGCCAGATTACCTGCG  
GCGCGGCTGGATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGA  
GTGCGCCGCGCGCGGGGCTGCCTGGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTG  
GGAATGCGCCAACCTCGAGGGCCAGCTCTGCGACCTGGACCCCACTGCTCACTTCTACGG  
GCACTGCGGCGAGCAGCTTGAGTGCCGGCTGGACACAGGCGGGCGACCTGAGCCGCGGAGA  
GGTGCCGGAACCTCTGTGTGCTGTGCTTCGCGAGAGTCCGCTCTGCGGGTCCGACGGTCA  
CACCTACTCCAGATCTGCCGCTGCAGGAGGCGGCCCCGCGCTCGGCCCGATGCCAACCT  
CACTGTGGCACACCCGGGGCCCTGCGAATCGGGGCCCCAGATCGTGTCACATCCATATGA  
CACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGTGAAGTGTTCCTACCCCAT  
GGCCTCCATCGAGTGAGGAAGGATGGCTTGACATCCAGCTGCCAGGGGATGACCCCCA  
CATCTCTGTGCAGTTTAGGGGTGGACCCAGAGGTTTGAGGTGACTGGCTGGCTGCAGAT  
CCAGGCTGTGCGTCCCAGTGATGAGGGCACTTACCGCTGCCTTGCCGCAATGCCCTGGG  
TCAAGTGAGGCCCCCTGCTAGCTTGACAGTGCTCACACCTGACCAGCTGAACTCTACAGG  
CATCCCCAGCTGCGATCACTAAACCTGGTTCCCTGAGGAGGAGGCTGAGAGTGAAGAGAA  
TGACGATTACTACTAGGTCCAGAGCTCTGGCCCATGGGGGTGGGTGAGCGGCTATAGTGT  
TCATCCCTGCTCTTGAAAAGACCTGGAAAGGGGAGCAGGGTCCCTTCATCGACTGCTTTC  
ATGCTGTGCTAGGGATGATCATGGGAGGCCTATTTGACTCCAAGGTAGCAGTGTGGTAG  
GATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAGACCAGGACCGGTGGGGTA  
CAAAGGGGCCCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCAACAGGTTGTTTCCCAG  
GCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGATTCTCCACTTCTTCC  
AGCCCTGCTGGGCCACAGTTCTAAGTGCCTTCCCTCCCAGGCCCTGGTTCTTGCTATTTTC  
CTGGTCCCCAACGTTTATCTAGCTTGTTTGCCCTTTCCCCAACTCATCTTCCAGAACTT  
TTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAAGTGCAGTCCCTTTTGCTGTCTGCCG  
TCTTTTGTACAAGAGAGAGAAACAGCGGAGCATGACTTAGTTCAGTGCAGAGAGATTT

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**FIGURE 366**

MLPPPRPAAALALPVLLLLLVLTTPPPTGARPSGPDYLRRGWMRLLAEGEGCAPCRPEE  
CAAPRGCLAGRVRDAGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRDLDGDLRGE  
VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSHPYD  
TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFVETGWLQI  
QAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN  
DDYY

**Important features of the protein:**

**Signal peptide:**

1-30

**Transmembrane domain:**

None

**N-glycosylation site:**

159-163, 183-187, 277-281

**Tyrosine kinase phosphorylation site:**

244-252

**N-myristoylation site:**

52-58, 66-72, 113-119, 249-255

**Kazal-type serine protease inhibitor domain:**

121-168

**Immunoglobulin domain:**

186-255

**Insulin-like growth factor binding proteins:**

53-90

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**FIGURE 367**

AGACGCTACAGGATGGAGCGGGGCGCAGGAGCCAAGCTGCTGCCGCTGCTGCTGCTTCTG  
CGGGCGACTGGTTTTACATGTGCACAGACAGATGGCCGGAACGGCTACACGGCGGTCATC  
GAAGTGACCAGCGGGGGTCCCTGGGGCGACTGGGCCTGGCCTGAGATGTGTCCCGATGGA  
TTCTTCGCCAGCGGGTTCTCGCTCAAGGTGGAGCCTCCCCAAGGCATTCTGGCGACGAC  
ACTGCACTGAATGGGATCAGGCTGCACTGCGCGCGCGGGAACGTCCTAGGCAATACGCAC  
GTGGTAGAGTCCAGTCTGGAAGCTGGGGCGAATGGAGTGAGCCGCTGTGGTGTGCGCGC  
GGCGCCTACCTAGTGGCTTTCTCGCTTCGCGTGGAGGCACCCACGACCCTCGGTGACAAC  
ACAGCAGCGAACAACGTGCGCTTCCGCTGTTTCAGACGGCGAGGAAGTGCAGGGGCCTGGG  
CTGAGCTGGGGAGACTTTGGAGACTGGAGTGACCATTGCCCAAGGGCGCGTGCGGCCTG  
CAGACCAAGATCCAGGGACCTAGAGGCCTCGGCGATGACACTGCGCTGAACGACGCGCGC  
TTATTCTGCTGCCGCAGTGAACGGCGCCGCCGCCGCTCTCTCCCGGGCCAGGAGGC  
TAGTCCCACCTCTTGCTATTAAAGCTTCTCTGAGTTG

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**FIGURE 368**

MERGAGAKLLPLLLLLLRATGFTCAQTDGRNGYTAVIEVTSGGPWGDWAWPEMCPDGFFAS  
GFSLKVEPPQGIPGDDTALNGIRLHCARGNVLGNTHVVESQSGSWGGEWSEPLWCRGGAYL  
VAFSLRVEAPTTLGDNNTAANNVRFRCSDEELQGPGLSWGDFGDWSDHCPKGACGLQTKI  
QGPRGLGDDTALNDARLFCCRS

Important features of the protein:

Signal peptide:

1-24

Transmembrane domain:

None

N-myristoylation site:

41-47

89-95

156-162

Growth factor and cytokines receptors family signature 2:

103-110

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## FIGURE 369

GCCAACACTGGCCAAACCTCGGAGACCGTCCTGCGCTCTCTGGAGACGCGCTGTCCGCGC  
CCAGGGTGGTGCCATGTGGGGCGCTCGCCGCTCGTCCGTCTCCTCATCCTGGAACGCCGC  
TTCGCTCCTGCAGCTGCTGCTGGCTGCGCTGCTGGCGGCGGGGGCGAGGGCCAGCGCGA  
GTACTGCCACGGCTGGCTGGACGCGCAGGGCGTCTGGCGCATCGGCTTCCAGTGTCCCGA  
GCGCTTCGACGGCGGGCGACGCCACCATCTGCTGCGGCAGCTGCGCGTTGCGCTACTGCTG  
CTCCAGCGCCGAGGCGCGCCTGGACCAGGGCGGCTGCGACAATGACCGCCAGCAGGGCGC  
TGGCGAGCCTGGCCGGGCGGACAAAGACGGCCCCGACGGCTCGGCAGTGCCCATCTACGT  
GCCGTTCCCTCATTTGTTGGCTCCGTGTTTGTGCGCTTTATCATCTTGGGGTCCCTGGTGGC  
AGCCTGTTGCTGCAGATGTCTCCGGCCTAAGCAGGATCCCCAGCAGAGCCGAGCCCCAGG  
GGGTAACCGCTTGATGGAGACCATCCCCATGATCCCCAGTGCCAGCACCTCCCGGGGGTC  
GTCCTCACGCCAGTCCAGCACAGCTGCCAGTTCCAGCTCCAGCGCCAACTCAGGGGCCCCG  
GGCGCCCCCAACAAGGTCACAGACCAACTGTTGCTTGCCGGAAGGGACCATGAACAACGT  
GTATGTCAACATGCCCACGAATTTCTCTGTGCTGAACTGTCAGCAGGCCACCCAGATTGT  
GCCACATCAAGGGCAGTATCTGCATCCCCCATACTGTTGGGTACACGGTGCAGCACGACTC  
TGTGCCCATGACAGCTGTGCCACCTTTCATGGACGGCCTGCAGCCTGGCTACAGGCAGAT  
TCAGTCCCCCTTCCCTCACACCAACAGTGAACAGAAGATGTACCCAGCGGTGACTGTATA  
ACCGAGAGTCACTGGTGGGTTCCTTTACTGAAGGGAGACGAAGGCAGGGGTGGATTTTCG  
AGGTGGAAGT

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**FIGURE 370**

MWGARRSSVSSSWNAASLLQLLLAALLAAGARASGEYCHGWLDAQGVWRIGFQCPERFDG  
GDATICCGSCALRYCCSSAEARLDQGGCDNDRQQGAGEPGRADKDGPDGSAVPIYVPFLI  
VGSVFVAFIILGSLVAACCCRCRLRPKQDPQQSRAPGGNRLMETIPMIPSASTSRGSSSRQ  
SSTAASSSSSANS GARAPPTRSQTNCCLPEGTMNNVYVNMPTNFSVLNCQQATQIVPHQG  
QYLHPPYVG YTVQHDSVPMTAVPPFMDGLQPGYRQIQSPFPHTNSEQKMYPAVTV

Important features of the protein: .

Signal peptide:

1-33

Transmembrane domain:

54-78

N-glycosylation site:

223-226

cAMP- and cGMP-dependent protein kinase phosphorylation site:

5-8

N-myristoylation site:

3-8, 30-35, 60-65, 86-91, 132-137, 211-216, 268-273

Prokaryotic membrane lipoprotein lipid attachment site:

128-138



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## FIGURE 371

CACCAGACAGCACTCCAGCACTCTGTTTTGGGGGGCATTTCGAAACAGCAAAATCACTCATA  
AAAGGCAAAAAATTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGA  
AAAGACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTCTAGCTTGTTC  
CCTCAGCTGGGAATGTGCATCAGGCAACTCAAGTTTTTCACCACGGCATGTGTCTGTGAA  
TGTCCGCAAAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACC  
TGGGCACTGTGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAG  
CCTGAGAACATTTCTGTGTCTACTACTATAGGAAAAATTTAACCTGCCTTGGAGTCCA  
GGAAAGGAAACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAA  
CATGATAATTGTACAACCAATAGTTCTACAAGTGAAAAATCGTGCTTCGTGCTCTTTTTC  
CTTCCAAGAATAACGATCCCAGATAATTATACCATGAGGTGGAAGCTGAAAAATGGAGAT  
GGTGTAATTAAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCA  
CCTAAGATTTTCCGTGTGAAACCAGTTTTTGGGCATCAAACGAATGATTCAAATTGAATGG  
ATAAAGCCTGAGTTGGCGCCTGTTTCATCTGATTTAAAAATACACACTTCGATTCAGGACA  
GTCAACAGTACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAAACCA  
ACGTACAACCTCACGGGGCTGCAGCCTTTTACAGAATATGTCTAGCTCTGCGATGTGCG  
GTCAAGGAGTCAAAGTCTGGAGTGACTGGAGCCAAGAAAAAATGGGAATGACTGAGGAA  
GAAGCTCCATGTGGCCTGGAACCTGTGGAGAGTCTGAAACCAGCTGAGGCGGATGGAAGA  
AGGCCAGTGCGTTGTTATGGAAGAAGGCAAGAGGAGCCCCAGTCTTAGAGAAAAACACTT  
GGCTACAACATATGGTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATGAACACT  
ACTAACAGCAGCTTGAACTGCATCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCT  
TATAATTCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAA  
TCATTTTCAGTGCATTGAGGTCTATGCAGGCGCTGCGTTGCTGAGGACCAGCTGGGTGAAG  
TGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGTTTCCGGATGTGGAC  
TCAGAGCCCACCACCTTTCTGGGAATCTGTGTCTCAGGCCACGAACCTGGACGATCCAG  
CAAGATAAATTAAAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGTCATGAC  
AAAGTTGGCGAGCCATATTCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGT  
CCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATT  
CCCAAGAGTGAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGT  
GGAAAAGGATTCTGTAAGCACGCCATAGCGAAGTGGAAGAAAAACCCCAAGCCCCAGATA  
GATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCCATCTCATTTGACTTGCAACCT  
GGCATGAATCACTTAGCTTCTTTAAATCTCTCTGAAAATGGGGCCAAGAGCACCCACCTT  
TTGGGGTTTTGGGGTTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGAGTCTGAGG  
AAATGGAAGGAGTTGTTATTAATTTGTCTGCTTAGGCCCTGAATTGACCTCCCGGGAGCT  
CCCCGACCATCATTCCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCC  
TGTCACCATGACTTCTACTGCCCCCTGCCAATCATGCTTTTGTTTTTTCAGTCCACCTTAT  
CTCCTGACATCTTAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTT  
CTTATGGTAAAATACACGTAAAAATTTTTCCAGTTTAAACATTTGAAAGTGTAATTTT  
AGTGGCATTAGAAGCATTACAATATTGTGCAACCATCACCCTATTTCCAGAACTCTTC  
TATTTCTGCCCAAATAGAAGCCCTATACCCATTATTAGTCACTCCCATTCCTCTCCTC  
CCACAGCCCCTGGCAACTACCAAACTGCTTTGTGTCTCTATGGATTGCCTATTTTGGATA  
TTTCATATACATAGAATCATAAANTAAAAA

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**FIGURE 372**

MCIRQLKFFTTACVCECPQNILSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENI  
SCVYYYRKNLTCTWSPGKETS YTQYTVKRTYAFGEKHDNCTTNSSTSENRASCSFFLPRI  
TIPDNYTIEVEAENG DGVIKSHMTYWRL ENIAKTEPPKIFRVKPV LGIKRMIQIEWIKPE  
LAPVSSDLKYTLRFRTVNSTSWMEVNF AKNRKDKNQTYNLTGLQPFTEYVIALRCAVKES  
KFWSDWSQEKMGMT EEEAPCGLELWRVLKPAEADGRRPVRL LWKKARGAPVLEKTLGYNI  
WYYPESNTNLTETMNTTNQQLHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKS FQC  
IEVMQACVAEDQLVVKWQSSALDVNTWMI EWFPD VDSEPTTLSWESVSQATNWTIQQDKL  
KPFWCYNISVYPMLHDKVGE PYSIQAYAKEGVPSEGPETKVENIGVKT VTTITWKEIPKSE  
RKGIIICNYTIFYQAEGGKGFC KHAHSEVEKNPKPQIDAMDRPVVGMAPP SHCDLQPGMNH  
LASLNLS ENGAKSTHLLGFWGLNESEVTV PERRVLRKWKELL

**Important features of the protein:****Signal peptide:**

1-46

**Transmembrane domain:**

None

**N-glycosylation site:**

59-63, 69-73, 99-103, 103-107, 125-129, 198-202, 215-219, 219-223, 309-313, 315-319, 412-416, 427-431, 487-491, 545-549, 563-567

**N-myristoylation site:**

32-38, 137-143, 483-489, 550-556, 561-567

**Amidation site:**

274-278

**Growth factor and cytokines receptors family signature 1:**

62-75

**Fibronectin type III domain:**

54-144

154-247

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## FIGURE 373

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCC  
CTCGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTG  
TGGACAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGC  
CCCAGCAAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCAC  
GCCTGGGCTCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCAC  
CACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCC  
ACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTG  
CTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGC  
CGTTAGGGTGTGTGCTGTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTTCGTGCAGC  
GTGTGTACCAGCCCTTCCTCACACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAA  
CCATTTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACG  
CGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTG  
CAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCG  
GCTGTCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGC  
ACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCC  
CCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGACAGAGGCTGCAGTCCAGGG  
TGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGC  
AGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGC  
TCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCTGGAGGAGCAGCTGGGGTCCT  
GCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCCTCACGC  
CGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGT  
GACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTCCCCTTCCCTCGGGAGG  
GTCCCCAGACCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAATCCACCCCTGGCTAC  
CCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGG  
TACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGG  
GTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGAAAA  
AAAGGGCGGCCGCGACTCTAGAGTC  
GACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAAT

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**FIGURE 374**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGD  
PVSESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGL  
PGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGS  
YWCQCWEGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVL  
APLHSLASQALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

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FIGURE 375

Wholemount In Situ with PRO1449 Orthologue

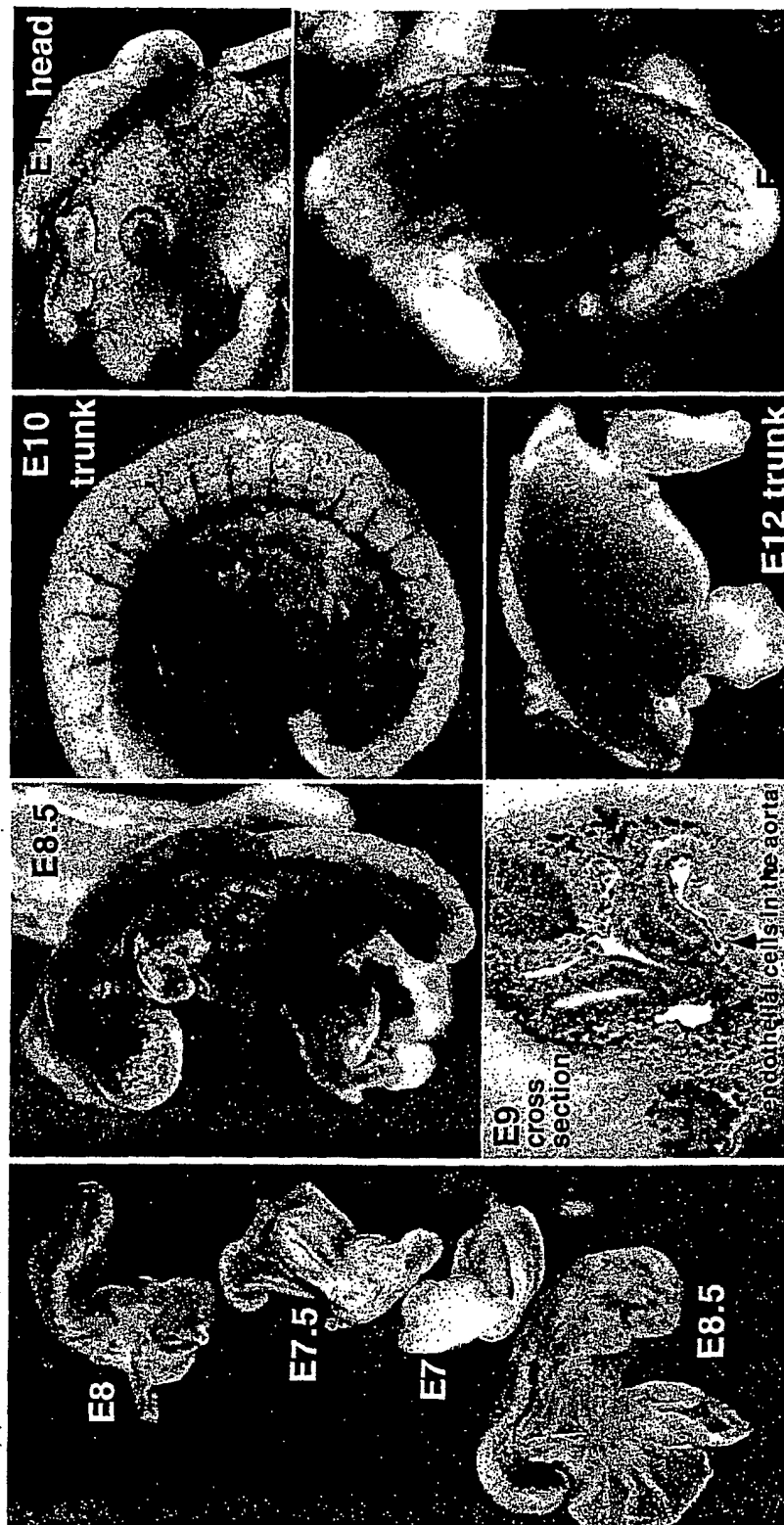
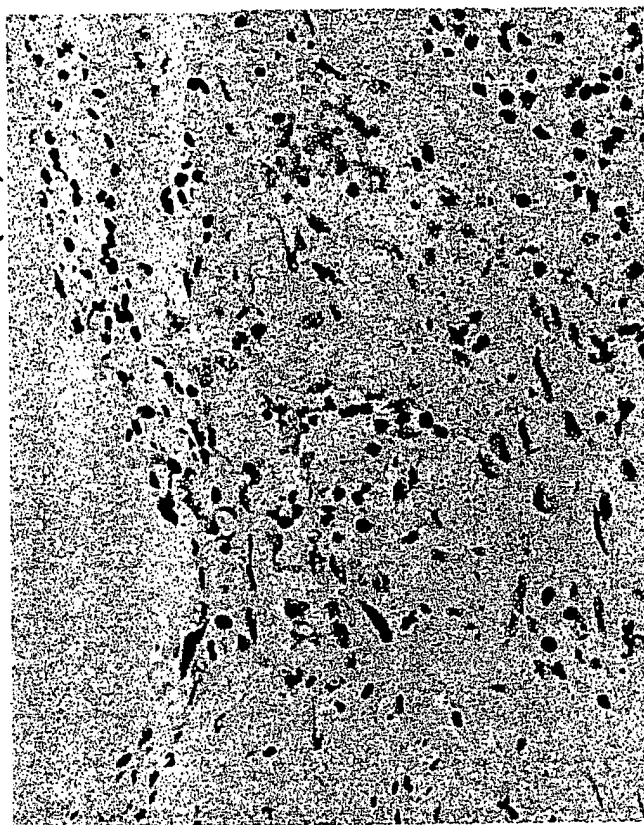


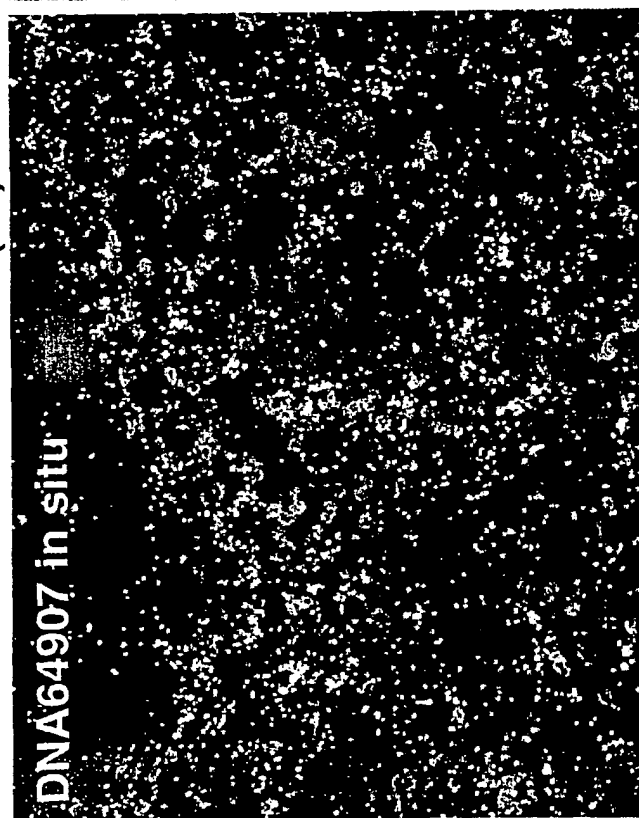
FIGURE 376

PRO1449 is expressed in vasculature of many inflamed and diseased tissues

Human tumor tissue (BF)



Human tumor tissue (DF)



DNA64907 in situ

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## FIGURE 377

Mouse orthologue of PRO1449 induces ectopic vessels in the eyes of chicken embryos

